

SEQUENCE LISTING

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 Nielsen, Tom
 Kauppinen, Markus
 Christensen, Soeren

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<170> PatentIn version 3.1

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Pro Thr Ile Leu Lys Asp Ala Phe Thr Asp Ile Leu Glu Asp Leu Gly
 335 340 345

Glu Arg Asn Asp Asp Ile Ala Val Tyr Ser Pro Asn Pro Phe Ser Gly
 350 355 360

Tyr Arg Asp Ser Ser Glu Asp Tyr Ala Thr Ala Lys Asp Leu Asp Val
 365 370 375

Val Asp Gly Gly Glu Asp Gly Glu Asn Ile Pro Leu His Pro Leu Ile
 380 385 390

Gln Pro Glu Arg Ala Val Asp Val Ile Phe Ala Ile Asp Ser Ser Ala
 395 400 405 410

Asp Thr Asp Tyr Tyr Trp Pro Asn Gly Thr Ser Leu Val Ala Thr Tyr
 415 420 425

Glu Arg Ser Leu Glu Pro Ser Ile Ala Asn Gly Thr Ala Phe Pro Ala
 430 435 440

Val Pro Asp Gln Asn Thr Phe Val Asn Leu Gly Leu Asn Ser Arg Pro
 445 450 455

Thr Phe Phe Gly Cys Asp Pro Lys Asn Ile Ser Gly Thr Ala Pro Leu
 460 465 470

Val Ile Tyr Leu Pro Asn Ser Pro Tyr Thr Tyr Asp Ser Asn Phe Ser
 475 480 485 490

Thr Phe Lys Leu Thr Tyr Ser Asp Glu Glu Arg Asp Ser Val Ile Thr
 495 500 505

Asn Gly Trp Asn Val Val Thr Arg Gly Asn Gly Thr Val Asp Asp Asn
 510 515 520

Phe Pro Ser Cys Val Ala Cys Ala Ile Leu Gln Ala Leu His Tyr Arg
 525 530 535

Thr Asn Thr Ser Leu Pro Asp Ile Cys Thr Thr Cys Phe Asn Asp Tyr
 540 545 550

Cys Trp Asn Gly Thr Thr Asn Ser Thr Thr Pro Gly Ala Tyr Glu Pro
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Ser Val Leu Ile Ala Thr Ser Gly Ala Ile Lys Ser Val Leu Asp Tyr
 575 580 585

Ser Val Leu Ala Leu Ala Met Gly Val Ala Ala Phe Met Leu
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 <213> Aspergillus oryzae

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48

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Ser Ile Ala Val Thr Pro Arg Ala Phe Pro Asn Ala Pro Asp Lys Tyr	
-5 -1 1 5	
gct ccc gca aat gtt tcc tgt ccg tcg act cgt ccc agt atc cgc agt	144
Ala Pro Ala Asn Val Ser Cys Pro Ser Thr Arg Pro Ser Ile Arg Ser	
10 15 20 25	
gcc gcc gcc ctg tcc acc agt gag aag gat tgg ttg caa gtg cgt cgg	192
Ala Ala Ala Leu Ser Thr Ser Glu Lys Asp Trp Leu Gln Val Arg Arg	
30 35 40	
aat gag acc ctt gaa ccc atg aag gat ttg ctc ggg cgg ctc aat cta	240
Asn Glu Thr Leu Glu Pro Met Lys Asp Leu Leu Gly Arg Leu Asn Leu	
45 50 55	
agc tcc ttt gat gcc tcg ggg tac att gac cgt cat aaa aac aat gca	288
Ser Ser Phe Asp Ala Ser Gly Tyr Ile Asp Arg His Lys Asn Asn Ala	
60 65 70	
tcg aat att cca aac gtg gcc att gcc gtt tca ggt ggt ggt tac cgc	336
Ser Asn Ile Pro Asn Val Ala Ile Ala Val Ser Gly Gly Gly Tyr Arg	
75 80 85	
gct ttg acc aat ggc gcg ggt gct atc aag gca ttc gat agt cgt acc	384
Ala Leu Thr Asn Gly Ala Gly Ala Ile Lys Ala Phe Asp Ser Arg Thr	
90 95 100 105	
tcc aac tcc aca gcc cgt gga cag ctc gga ggc ctt ctg cag tcc tct	432
Ser Asn Ser Thr Ala Arg Gly Gln Leu Gly Gly Leu Leu Gln Ser Ser	
110 115 120	
act tat cta tcg ggc ctc agt ggt ggt gga tgg ctc gtg ggc tcc gtg	480
Thr Tyr Leu Ser Gly Leu Ser Gly Gly Gly Trp Leu Val Gly Ser Val	
125 130 135	
tac atc aac aac ttc acc act atc ggt gac ctg cag gcc agc gac aag	528
Tyr Ile Asn Asn Phe Thr Thr Ile Gly Asp Leu Gln Ala Ser Asp Lys	
140 145 150	
gtc tgg gac ttc aag aac tct att ctg gag ggt cct gat gtt aaa cat	576
Val Trp Asp Phe Lys Asn Ser Ile Leu Glu Gly Pro Asp Val Lys His	
155 160 165	
ttc caa ctg atc aac act gcc gcg tac tgg aag gat ctg tac gat gcg	624
Phe Gln Leu Ile Asn Thr Ala Ala Tyr Trp Lys Asp Leu Tyr Asp Ala	
170 175 180 185	
gtg aag gat aag aga aac gcc ggg ttc aac act tcg ttg acc gac tac	672
Val Lys Asp Lys Arg Asn Ala Gly Phe Asn Thr Ser Leu Thr Asp Tyr	
190 195 200	
tgg ggc cgt gct ctc tcc tat cag ttc atc aac gct acc act gat gat	720
Trp Gly Arg Ala Leu Ser Tyr Gln Phe Ile Asn Ala Thr Thr Asp Asp	

205	210	215	
ggc ggt ccc agt tat acc tgg tgc tgc att gcc ttg ggc gac gat ttc Gly Gly Pro Ser Tyr Thr Trp Ser Ser Ile Ala Leu Gly Asp Asp Phe 220 225 230			768
aag aag ggc aag atg ccc atg cct atc ctc gtc gcc gat gga cgt aac Lys Lys Gly Lys Met Pro Met Pro Ile Leu Val Ala Asp Gly Arg Asn 235 240 245			816
ccg ggc gaa ata ctt att gga agt aac tgc act gtg tat gaa ttt aac Pro Gly Glu Ile Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn 250 255 260 265			864
cca tgg gag ttc ggc tcc ttc gac ccg tca gta tac ggc ttt gca cca Pro Trp Glu Phe Gly Ser Phe Asp Pro Ser Val Tyr Gly Phe Ala Pro 270 275 280			912
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agc tct tcc ctg ttt aac cag ttc att ctg cgt ctg aac ggc acc gat Ser Ser Ser Leu Phe Asn Gln Phe Ile Leu Arg Leu Asn Gly Thr Asp 315 320 325			1056
atc cct aat ttc ctc aag gag gcg att gcc gac gtc ttg gaa cat ctg Ile Pro Asn Phe Leu Lys Glu Ala Ile Ala Asp Val Leu Glu His Leu 330 335 340 345			1104
ggc gaa aac gat gag gac att gca gtt tac gca ccc aac ccc ttc tac Gly Glu Asn Asp Glu Asp Ile Ala Val Tyr Ala Pro Asn Pro Phe Tyr 350 355 360			1152
aaa tat cgc aat tca acg gca gca tat tgc tca acc cca gag ctg gac Lys Tyr Arg Asn Ser Thr Ala Ala Tyr Ser Ser Thr Pro Glu Leu Asp 365 370 375			1200
gtg gtc gac gga ggt gaa gat gga cag aac gtg cct cta cac ccg ttg Val Val Asp Gly Gly Glu Asp Gly Gln Asn Val Pro Leu His Pro Leu 380 385 390			1248
atc cag ccc acc cac aac gtg gat gtg atc ttt gcc gtg gat tgc tcc Ile Gln Pro Thr His Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser 395 400 405			1296
gct gat acg gac cat agc tgg ccc aac gga tcc tcc ttg atc tac acc Ala Asp Thr Asp His Ser Trp Pro Asn Gly Ser Ser Leu Ile Tyr Thr 410 415 420 425			1344
tat gaa cgt agc ttg aat act aca ggt atc gcc aac ggg acc tcc ttc Tyr Glu Arg Ser Leu Asn Thr Thr Gly Ile Ala Asn Gly Thr Ser Phe 430 435 440			1392

cct gcg gtg ccc gac gtc aac acg ttc ctc aac ctt ggc ctg aac aaa	1440
Pro Ala Val Pro Asp Val Asn Thr Phe Leu Asn Leu Gly Leu Asn Lys	
445 450 455	
cgc ccg acc ttc ttc gga tgc aat tca tcc aac acc agc acc ccg acc	1488
Arg Pro Thr Phe Phe Gly Cys Asn Ser Ser Asn Thr Ser Thr Pro Thr	
460 465 470	
cca ttg att gtc tac ttg ccc aac gcc cct tac acc gcc gag tcc aac	1536
Pro Leu Ile Val Tyr Leu Pro Asn Ala Pro Tyr Thr Ala Glu Ser Asn	
475 480 485	
acg tca acc ttc cag ctg gcg tat aag gac caa caa cgc gat gat att	1584
Thr Ser Thr Phe Gln Leu Ala Tyr Lys Asp Gln Gln Arg Asp Asp Ile	
490 495 500 505	
atc ttg aac ggc tac aac gtc gtc acc cag ggc aat gcc agt gcc gat	1632
Ile Leu Asn Gly Tyr Asn Val Val Thr Gln Gly Asn Ala Ser Ala Asp	
510 515 520	
gca aac tgg ccc tcg tgc gtt ggg tgc gct att ctc cag cgg tcc acc	1680
Ala Asn Trp Pro Ser Cys Val Gly Cys Ala Ile Leu Gln Arg Ser Thr	
525 530 535	
gaa cgt acg aac act aag ctt ccc gat atc tgc aat acc tgc ttc aag	1728
Glu Arg Thr Asn Thr Lys Leu Pro Asp Ile Cys Asn Thr Cys Phe Lys	
540 545 550	
aat tac tgc tgg gac gga aag acc aac agc acc aca ccg gcc ccc tat	1776
Asn Tyr Cys Trp Asp Gly Lys Thr Asn Ser Thr Thr Pro Ala Pro Tyr	
555 560 565	
gaa ccg gag cta ttg atg gag gcg tcg act tcc ggg gcc tcg aag gat	1824
Glu Pro Glu Leu Leu Met Glu Ala Ser Thr Ser Gly Ala Ser Lys Asp	
570 575 580 585	
caa ctg aac cgg aca gct gca gtc atc gcg ttc gca gtt atg ttc ttt	1872
Gln Leu Asn Arg Thr Ala Ala Val Ile Ala Phe Ala Val Met Phe Phe	
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atg acg atc tag	1884
Met Thr Ile	

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 <212> PRT
 <213> *Aspergillus oryzae*

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 -5 -1 1 5

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Ala Ala Ala Leu Ser Thr Ser Glu Lys Asp Trp Leu Gln Val Arg Arg
 30 35 40

Asn Glu Thr Leu Glu Pro Met Lys Asp Leu Leu Gly Arg Leu Asn Leu
 45 50 55

Ser Ser Phe Asp Ala Ser Gly Tyr Ile Asp Arg His Lys Asn Asn Ala
 60 65 70

Ser Asn Ile Pro Asn Val Ala Ile Ala Val Ser Gly Gly Gly Tyr Arg
 75 80 85

Ala Leu Thr Asn Gly Ala Gly Ala Ile Lys Ala Phe Asp Ser Arg Thr
 90 95 100 105

Ser Asn Ser Thr Ala Arg Gly Gln Leu Gly Gly Leu Leu Gln Ser Ser
 110 115 120

Thr Tyr Leu Ser Gly Leu Ser Gly Gly Gly Trp Leu Val Gly Ser Val
 125 130 135

Tyr Ile Asn Asn Phe Thr Thr Ile Gly Asp Leu Gln Ala Ser Asp Lys
 140 145 150

Val Trp Asp Phe Lys Asn Ser Ile Leu Glu Gly Pro Asp Val Lys His
 155 160 165

Phe Gln Leu Ile Asn Thr Ala Ala Tyr Trp Lys Asp Leu Tyr Asp Ala
 170 175 180 185

Val Lys Asp Lys Arg Asn Ala Gly Phe Asn Thr Ser Leu Thr Asp Tyr
 190 195 200

Trp Gly Arg Ala Leu Ser Tyr Gln Phe Ile Asn Ala Thr Thr Asp Asp
 205 210 215

Gly Gly Pro Ser Tyr Thr Trp Ser Ser Ile Ala Leu Gly Asp Asp Phe

220	225	230
Lys Lys Gly Lys Met Pro Met Pro Ile Leu Val Ala Asp Gly Arg Asn 235 240 245		
Pro Gly Glu Ile Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn 250 255 260 265		
Pro Trp Glu Phe Gly Ser Phe Asp Pro Ser Val Tyr Gly Phe Ala Pro 270 275 280		
Leu Glu Tyr Leu Gly Ser Asn Phe Glu Asn Gly Glu Leu Pro Lys Gly 285 290 295		
Glu Ser Cys Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr 300 305 310		
Ser Ser Ser Leu Phe Asn Gln Phe Ile Leu Arg Leu Asn Gly Thr Asp 315 320 325		
Ile Pro Asn Phe Leu Lys Glu Ala Ile Ala Asp Val Leu Glu His Leu 330 335 340 345		
Gly Glu Asn Asp Glu Asp Ile Ala Val Tyr Ala Pro Asn Pro Phe Tyr 350 355 360		
Lys Tyr Arg Asn Ser Thr Ala Ala Tyr Ser Ser Thr Pro Glu Leu Asp 365 370 375		
Val Val Asp Gly Gly Glu Asp Gly Gln Asn Val Pro Leu His Pro Leu 380 385 390		
Ile Gln Pro Thr His Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser 395 400 405		
Ala Asp Thr Asp His Ser Trp Pro Asn Gly Ser Ser Leu Ile Tyr Thr 410 415 420 425		
Tyr Glu Arg Ser Leu Asn Thr Thr Gly Ile Ala Asn Gly Thr Ser Phe 430 435 440		
Pro Ala Val Pro Asp Val Asn Thr Phe Leu Asn Leu Gly Leu Asn Lys 445 450 455		

Arg Pro Thr Phe Phe Gly Cys Asn Ser Ser Asn Thr Ser Thr Pro Thr
 460 465 470

Pro Leu Ile Val Tyr Leu Pro Asn Ala Pro Tyr Thr Ala Glu Ser Asn
 475 480 485

Thr Ser Thr Phe Gln Leu Ala Tyr Lys Asp Gln Gln Arg Asp Asp Ile
 490 495 500 505

Ile Leu Asn Gly Tyr Asn Val Val Thr Gln Gly Asn Ala Ser Ala Asp
 510 515 520

Ala Asn Trp Pro Ser Cys Val Gly Cys Ala Ile Leu Gln Arg Ser Thr
 525 530 535

Glu Arg Thr Asn Thr Lys Leu Pro Asp Ile Cys Asn Thr Cys Phe Lys
 540 545 550

Asn Tyr Cys Trp Asp Gly Lys Thr Asn Ser Thr Thr Pro Ala Pro Tyr
 555 560 565

Glu Pro Glu Leu Leu Met Glu Ala Ser Thr Ser Gly Ala Ser Lys Asp
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Gln Leu Asn Arg Thr Ala Ala Val Ile Ala Phe Ala Val Met Phe Phe
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Met Thr Ile

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 <213> *Aspergillus oryzae*

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Met Lys Pro Thr Thr Ala Ala Ile Ala Leu Ala
-35 -30
ggg ttg ctg tct ggc gtg aca gcg gcc cca ggc cct cat gga gaa agg 159
Gly Leu Leu Ser Gly Val Thr Ala Ala Pro Gly Pro His Gly Glu Arg
-25 -20 -15
att gag agg att gat aga act gtg ttg gaa cgt gca ttg cca aat gct 207
Ile Glu Arg Ile Asp Arg Thr Val Leu Glu Arg Ala Leu Pro Asn Ala
-10 -5 -1 1 5
ccc gat gga tat gta ccg tcc aac gtc agt tgt cct gcg aat cgc ccg 255
Pro Asp Gly Tyr Val Pro Ser Asn Val Ser Cys Pro Ala Asn Arg Pro
10 15 20
acg gtg cgt agc gca tca tcc ggg ctc tcg agc aat gag acc tcg tgg 303
Thr Val Arg Ser Ala Ser Ser Gly Leu Ser Ser Asn Glu Thr Ser Trp
25 30 35
ttg aaa acc cga cgg gag aag act caa tct gcc atg aaa gat ttc ttc 351
Leu Lys Thr Arg Arg Glu Lys Thr Gln Ser Ala Met Lys Asp Phe Phe
40 45 50
aac cat gtc acg att aag gac ttt gat gct gtc caa tat ctc gac aac 399
Asn His Val Thr Ile Lys Asp Phe Asp Ala Val Gln Tyr Leu Asp Asn
55 60 65
cac tcg agt aac acg tcc aat ctt ccc aat att ggt att gcg gtg tct 447
His Ser Ser Asn Thr Ser Asn Leu Pro Asn Ile Gly Ile Ala Val Ser
70 75 80 85
ggg gga ggt tat cgc gcc ctg atg aac ggt gcc gga gcg atc aaa gcg 495
Gly Gly Gly Tyr Arg Ala Leu Met Asn Gly Ala Gly Ala Ile Lys Ala
90 95 100
ttt gat agc cga acg gag aac tcg acg gcg acg gga cag ttg ggt ggt 543
Phe Asp Ser Arg Thr Glu Asn Ser Thr Ala Thr Gly Gln Leu Gly Gly
105 110 115
ctg cta cag tcg gcg acg tat ctg gct ggt ctg agt ggt ggt gga tgg 591
Leu Leu Gln Ser Ala Thr Tyr Leu Ala Gly Leu Ser Gly Gly Gly Trp
120 125 130
ctg gtg ggg tcg atc tat atc aac aat ttc acc acc att tca gca ctg 639
Leu Val Gly Ser Ile Tyr Ile Asn Asn Phe Thr Thr Ile Ser Ala Leu
135 140 145
cag acc cat gag gat ggt gct gtc tgg cag ttt caa aac tcg att ttt 687
Gln Thr His Glu Asp Gly Ala Val Trp Gln Phe Gln Asn Ser Ile Phe
150 155 160 165

gag ggc cct gac ggc gat agc att cag att ctg gat tct gcg act tac	735
Glu Gly Pro Asp Gly Asp Ser Ile Gln Ile Leu Asp Ser Ala Thr Tyr	
170 175 180	
tac aag cac gtt tac gat gca gtg caa gac aag aag gat gcg gga tac	783
Tyr Lys His Val Tyr Asp Ala Val Gln Asp Lys Lys Asp Ala Gly Tyr	
185 190 195	
gaa acc tct atc act gat tat tgg ggt cgc gct ctc tct tat caa tta	831
Glu Thr Ser Ile Thr Asp Tyr Trp Gly Arg Ala Leu Ser Tyr Gln Leu	
200 205 210	
atc aat gct acc gac ggc ggt ccg agc tat act tgg tcg tcc att gcc	879
Ile Asn Ala Thr Asp Gly Gly Pro Ser Tyr Thr Trp Ser Ser Ile Ala	
215 220 225	
cta acc gat aca ttt aag cag gca gat atg ccg atg cct ctc ctc gtt	927
Leu Thr Asp Thr Phe Lys Gln Ala Asp Met Pro Met Pro Leu Leu Val	
230 235 240 245	
gcc gac ggt cgg tat ccc gat gag ctc gtg gtc agc agc aac gct act	975
Ala Asp Gly Arg Tyr Pro Asp Glu Leu Val Val Ser Ser Asn Ala Thr	
250 255 260	
gtc tat gag ttt aac cct tgg gag ttt ggt act ttt gat cca aca gtc	1023
Val Tyr Glu Phe Asn Pro Trp Glu Phe Gly Thr Phe Asp Pro Thr Val	
265 270 275	
tac ggg ttt gtg cct cta gaa tac gta ggc tct aaa ttc gac ggt ggt	1071
Tyr Gly Phe Val Pro Leu Glu Tyr Val Gly Ser Lys Phe Asp Gly Gly	
280 285 290	
tct atc ccc gac aac gag acc tgt gta cgc gga ttc gac aac gcc ggt	1119
Ser Ile Pro Asp Asn Glu Thr Cys Val Arg Gly Phe Asp Asn Ala Gly	
295 300 305	
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Phe Val Met Gly Thr Ser Ser Ser Leu Phe Asn Gln Phe Phe Leu Gln	
310 315 320 325	
gtt aac tca act tcg ctt cct gat ttc ctg aag acg gca ttc tcg gac	1215
Val Asn Ser Thr Ser Leu Pro Asp Phe Leu Lys Thr Ala Phe Ser Asp	
330 335 340	
atc ttg gca aag att ggt gaa gaa gat gag gac att gct gtc tat gca	1263
Ile Leu Ala Lys Ile Gly Glu Glu Asp Glu Asp Ile Ala Val Tyr Ala	
345 350 355	
ccc aac ccg ttc tac aat tgg gcc ccc gtg agc tca cca gca gcc cat	1311
Pro Asn Pro Phe Tyr Asn Trp Ala Pro Val Ser Ser Pro Ala Ala His	
360 365 370	
caa cag gaa ctc gat atg gtg gac ggt ggc gag gat ctt cag aac att	1359
Gln Gln Glu Leu Asp Met Val Asp Gly Gly Glu Asp Leu Gln Asn Ile	
375 380 385	
cct ctg cat cct tta att cag cca gag cgt cac gta gat gtt atc ttt	1407

Pro Leu His Pro Leu Ile Gln Pro Glu Arg His Val Asp Val Ile Phe 390 395 400 405	
gct gtt gac tcc tcc gcc gac acg act tat tct tgg ccc aac ggc aca Ala Val Asp Ser Ser Ala Asp Thr Thr Tyr Ser Trp Pro Asn Gly Thr 410 415 420	1455
gct ctc gtt gcc act tac gag cgc agc ctg aac tcc acc ggc atc gct Ala Leu Val Ala Thr Tyr Glu Arg Ser Leu Asn Ser Thr Gly Ile Ala 425 430 435	1503
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acc aca ggc cct acg cct ttg gtt gtc tac ctt ccg aac tat cca tac Thr Thr Gly Pro Thr Pro Leu Val Val Tyr Leu Pro Asn Tyr Pro Tyr 470 475 480 485	1647
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ctg agt cgg tct ttc gag cgc acg aac acc cag gtt ccg gat gcc tgc Leu Ser Arg Ser Phe Glu Arg Thr Asn Thr Gln Val Pro Asp Ala Cys 535 540 545	1839
acc cag tgc ttc cag aag tac tgc tgg gat ggc act acg aac tcc acc Thr Gln Cys Phe Gln Lys Tyr Cys Trp Asp Gly Thr Thr Asn Ser Thr 550 555 560 565	1887
aac cct gcc gac tat gag cct gtc acc ctg ttg gag gat agt gct ggt Asn Pro Ala Asp Tyr Glu Pro Val Thr Leu Leu Glu Asp Ser Ala Gly 570 575 580	1935
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ttttttttctc ttttctcttc ccaggaacta cttttatata tattgcgata tatcccgact	2091

tttttttttg cttctcttca atttcttcct cctgtgcctt ttagcttgat tgtatttaag 2151
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 aaaaaaaaaa aaaaaaaaaa aa 2233

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 <211> 641
 <212> PRT
 <213> *Aspergillus oryzae*

<400> 8

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 -20 -15 -10

Arg Thr Val Leu Glu Arg Ala Leu Pro Asn Ala Pro Asp Gly Tyr Val
 -5 -1 1 5 10

Pro Ser Asn Val Ser Cys Pro Ala Asn Arg Pro Thr Val Arg Ser Ala
 15 20 25

Ser Ser Gly Leu Ser Ser Asn Glu Thr Ser Trp Leu Lys Thr Arg Arg
 30 35 40

Glu Lys Thr Gln Ser Ala Met Lys Asp Phe Phe Asn His Val Thr Ile
 45 50 55

Lys Asp Phe Asp Ala Val Gln Tyr Leu Asp Asn His Ser Ser Asn Thr
 60 65 70

Ser Asn Leu Pro Asn Ile Gly Ile Ala Val Ser Gly Gly Gly Tyr Arg
 75 80 85 90

Ala Leu Met Asn Gly Ala Gly Ala Ile Lys Ala Phe Asp Ser Arg Thr
 95 100 105

Glu Asn Ser Thr Ala Thr Gly Gln Leu Gly Gly Leu Leu Gln Ser Ala
 110 115 120

Thr Tyr Leu Ala Gly Leu Ser Gly Gly Gly Trp Leu Val Gly Ser Ile
 125 130 135

Tyr Ile Asn Asn Phe Thr Thr Ile Ser Ala Leu Gln Thr His Glu Asp
 140 145 150

Gly Ala Val Trp Gln Phe Gln Asn Ser Ile Phe Glu Gly Pro Asp Gly
 155 160 165 170

Asp Ser Ile Gln Ile Leu Asp Ser Ala Thr Tyr Tyr Lys His Val Tyr
 175 180 185

Asp Ala Val Gln Asp Lys Lys Asp Ala Gly Tyr Glu Thr Ser Ile Thr
 190 195 200

Asp Tyr Trp Gly Arg Ala Leu Ser Tyr Gln Leu Ile Asn Ala Thr Asp
 205 210 215

Gly Gly Pro Ser Tyr Thr Trp Ser Ser Ile Ala Leu Thr Asp Thr Phe
 220 225 230

Lys Gln Ala Asp Met Pro Met Pro Leu Leu Val Ala Asp Gly Arg Tyr
 235 240 245 250

Pro Asp Glu Leu Val Val Ser Ser Asn Ala Thr Val Tyr Glu Phe Asn
 255 260 265

Pro Trp Glu Phe Gly Thr Phe Asp Pro Thr Val Tyr Gly Phe Val Pro
 270 275 280

Leu Glu Tyr Val Gly Ser Lys Phe Asp Gly Gly Ser Ile Pro Asp Asn
 285 290 295

Glu Thr Cys Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr
 300 305 310

Ser Ser Ser Leu Phe Asn Gln Phe Phe Leu Gln Val Asn Ser Thr Ser
 315 320 325 330

Leu Pro Asp Phe Leu Lys Thr Ala Phe Ser Asp Ile Leu Ala Lys Ile
 335 340 345

Gly Glu Glu Asp Glu Asp Ile Ala Val Tyr Ala Pro Asn Pro Phe Tyr
 350 355 360

Asn Trp Ala Pro Val Ser Ser Pro Ala Ala His Gln Gln Glu Leu Asp
365 370 375

Met Val Asp Gly Gly Glu Asp Leu Gln Asn Ile Pro Leu His Pro Leu
380 385 390

Ile Gln Pro Glu Arg His Val Asp Val Ile Phe Ala Val Asp Ser Ser
395 400 405 410

Ala Asp Thr Thr Tyr Ser Trp Pro Asn Gly Thr Ala Leu Val Ala Thr
415 420 425

Tyr Glu Arg Ser Leu Asn Ser Thr Gly Ile Ala Asn Gly Thr Ser Phe
430 435 440

Pro Ala Ile Pro Asp Gln Asn Thr Phe Val Asn Asn Gly Leu Asn Thr
445 450 455

Arg Pro Thr Phe Phe Gly Cys Asn Ser Thr Asn Thr Thr Gly Pro Thr
460 465 470

Pro Leu Val Val Tyr Leu Pro Asn Tyr Pro Tyr Val Ser Tyr Ser Asn
475 480 485 490

Trp Ser Thr Phe Gln Pro Ser Tyr Glu Ile Ser Glu Arg Asp Asp Thr
495 500 505

Ile Arg Asn Gly Tyr Asp Val Val Thr Met Gly Asn Ser Thr Arg Asp
510 515 520

Gly Asn Trp Thr Thr Cys Val Gly Cys Ala Ile Leu Ser Arg Ser Phe
525 530 535

Glu Arg Thr Asn Thr Gln Val Pro Asp Ala Cys Thr Gln Cys Phe Gln
540 545 550

Lys Tyr Cys Trp Asp Gly Thr Thr Asn Ser Thr Asn Pro Ala Asp Tyr
555 560 565 570

Glu Pro Val Thr Leu Leu Glu Asp Ser Ala Gly Ser Ala Leu Ser Pro
575 580 585

Ala Val Ile Thr Thr Ile Val Ala Thr Ser Ala Ala Leu Phe Thr Leu

590

595

600

Leu

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<213> Artificial Sequence

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<223> Primer

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<222> (9)..(9)
<223> n denotes any nucleotide

<220>
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<223> HU175

<400> 9
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30

<210> 10
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Gly	Lys	Lys	Asn	Ala	Ala
			20		